

1647

12/27/00

#4

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/622,439

DATE: 12/27/2000

TIME: 13:41:01

Input Set : A:\Y04-12-1.app

Output Set: N:\CRF3\12272000\1622439.raw

ENTERED

1 <110> APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.

5 <120> TITLE OF INVENTION: A novel G protein coupled receptor protein

7 <130> FILE REFERENCE: Y9905

C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/622,439

C--> 10 <141> CURRENT FILING DATE: 2000-08-17

12 <150> PRIOR APPLICATION NUMBER: JP P1998-060215

13 <151> PRIOR FILING DATE: 1998-03-12

15 <150> PRIOR APPLICATION NUMBER: JP P1999-026771

16 <151> PRIOR FILING DATE: 1999-02-03

18 <160> NUMBER OF SEQ ID NOS: 26

20 <170> SOFTWARE: PatentIn Ver. 2.0

22 <210> SEQ ID NO: 1

23 <211> LENGTH: 1128

24 <212> TYPE: DNA

25 <213> ORGANISM: Homo sapiens

27 <220> FEATURE:

28 <221> NAME/KEY: CDS

29 <222> LOCATION: (1)..(1125)

36 <223> OTHER INFORMATION: SREEL

32 <400> SEQUENCE: 1

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34  Met  Ala  Asn  Ala  Ser  Glu  Pro  Gly-Gly  Ser  Gly  Gly  Gly  Glu  Ala  Ala
35      1              5              10              15
36  ggc  ctg  ggc  ctc  aag  ctg  gcc  acg  ctc  agc  ctg  ctg  ctg  tgc  gtg  agc  96
37  Ala  Leu  Gly  Leu  Lys  Leu  Ala  Phe  Leu  Ser  Leu  Leu  Leu  Cys  Val  Ser
38      20              25              30
39  cta  gcc  ggc  aac  gtg  ctg  ttc  ggc  ctg  ctg  atc  gtg  cgc  gag  cgc  agc  144
40  Leu  Ala  Gly  Asn  Val  Leu  Phe  Ala  Leu  Leu  Ile  Val  Arg  Glu  Arg  Ser
41      35              40              45
42  ctg  cgc  ggc  gcc  cgc  tac  tac  ctg  ctg  ctg  gac  ctg  tgc  ctg  gcc  gac  192
43  Leu  His  Arg  Ala  Pro  Tyr  Tyr  Leu  Leu  Leu  Asp  Leu  Cys  Leu  Ala  Asp
44      50              55              60
45  ggc  ctg  cgc  ggc  ctc  gcc  tgc  ctc  gcc  gcc  gtc  atg  ctg  gcc  gcc  cgc  240
46  Gly  Leu  Arg  Ala  Leu  Ala  Cys  Leu  Pro  Ala  Val  Met  Leu  Ala  Ala  Arg
47      65              70              75              80
48  cgt  gcc  gcc  gcc  gcc  gcc  gcc  gcc  gcc  gcc  gcc  ctg  gcc  tgc  aag  288
49  Arg  Ala  Ala  Ala  Ala  Ala  Gly  Ala  Pro  Pro  Gly  Ala  Leu  Gly  Cys  Lys
50      85              90              95
51  ctg  ctc  gcc  ttc  ctg  gcc  gcc  ctc  ttc  tgc  ctc  cgc  gcc  gcc  ttc  ctg  336
52  Leu  Leu  Ala  Phe  Leu  Ala  Ala  Leu  Phe  Cys  Phe  His  Ala  Ala  Phe  Leu
53      100             105             110
54  ctg  ctg  gcc  gtg  gcc  gtc  gcc  cgc  tac  ctg  gcc  atc  gcc  cgc  cgc  cgc  384
55  Leu  Leu  Gly  Val  Gly  Val  Thr  Arg  Tyr  Leu  Ala  Ile  Ala  His  His  Arg
56      115             120             125
57  ttc  tat  gcc  gag  cgc  ctg  gcc  gcc  tac  gcc  gcc  atg  ctg  ctg  432
58  Phe  Tyr  Ala  Glu  Arg  Leu  Ala  Gly  Trp  Pro  Cys  Ala  Ala  Met  Leu  Val
59      130             135             140

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69  tgc gcc gcc tgg gcc ctg gcc ctg gcc gcc gcc ttc ccg cca gtc ctg 480
70  Cys Ala Ala Trp Ala Leu Ala Leu Ala Ala Ala Phe Pro Pro Val Leu
71  145 150 155 160
72  gcc gcc ggt gcc gcc gcc gcc gcc gcc tgc gcc ctg gag cag cgg 528
73  Asp Gly Gly Asp Asp Glu Asp Ala Pro Cys Ala Leu Glu Gln Arg
74  165 170 175
75  gcc gcc gcc gcc gcc gcc gcc ctg gcc ttc ctg ctg ctg ctg gcc ctg 576
76  Pro Asp Gly Ala Pro Gly Ala Leu Gly Phe Leu Leu Leu Leu Ala Val
77  180 185 190
78  gtc gtc gcc gcc acc gcc ctc gtc ttc ctc ctc ctc ttc ttc ttc 624
79  Val Val Gly Ala Thr His Leu Val Tyr Leu Arg Leu Leu Phe Phe Ile
80  195 200 205
81  gcc gcc gcc gcc gcc gcc gcc ctg gcc ctc gtc gcc gcc gcc gcc 672
82  His Asp Arg Arg Lys Met Arg Pro Ala Arg Leu Val Pro Ala Val Ser
83  210 215 220
84  gcc gcc tgg gcc gcc ttc gcc gcc gcc gcc gcc gcc gcc gcc gcc 720
85  His Asp Trp Thr Phe His Gly Pro Gly Ala Thr Gly Glu Ala Ala Ala
86  225 230 235 240
87  gcc gcc gcc gcc gcc gcc gcc gcc gcc gcc gcc gcc gcc gcc gcc 768
88  Asn Trp Thr Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Ala Leu Val
89  245 250 255
90  gcc gcc gcc gcc gcc gcc gcc gcc gcc gcc gcc gcc gcc gcc gcc 816
91  Gly Ile Arg Pro Ala Gly Pro Gly Arg Gly Ala Arg Arg Leu Leu Val
92  260 265 270
93  ctg gaa gaa ttc aag aag gag aag aag ctg tgc aag atg ttc tac gcc 864
94  Leu Glu Glu Phe Lys Thr Glu Lys Arg Leu Cys Lys Met Phe Tyr Ala
95  275 280 285
96  gtc acc ctg ctg ttc ctg ctg ctg tgg gcc gcc ttc gtc gtc gcc gcc 912
97  Val Thr Leu Leu Phe Leu Leu Leu Trp Gly Pro Tyr Val Val Ala Ser
98  290 295 300
99  ttc ctg gcc gtc ctg gtc gcc gcc gcc gcc gcc gcc gcc gcc gcc 960
100 Tyr Leu Arg Val Leu Val Arg Pro Gly Ala Val Pro Glu Ala Tyr Leu
101 305 310 315 320
102 acc gcc ttc gtc tgg ctg acc ttc ggc cag gcc gcc gcc gcc gcc 1008
103 Thr Ala Ser Val Trp Leu Thr Phe Ala Glu Ala Gly Ile Asn Pro Val
104 325 330 335
105 gtc tgc ttc ctc ttc aac agg gag ctg agg gcc tgc ttc agg gcc cag 1056
106 Val Cys Phe Leu Phe Asn Arg Glu Leu Arg Asp Cys Phe Arg Ala Glu
107 340 345 350
108 ttc gcc tgc tgc cag gcc gcc gcc gcc gcc gcc gcc gcc gcc gcc 1104
109 Phe Pro Cys Cys Glu Ser Pro Arg Thr Thr Glu Ala Thr His Pro Cys
110 355 360 365
111 gcc ctg aac gcc att ggt tta tga 1128
112 Asp Leu Lys Gly Ile Gly Leu
113 370 375
114 <210> SEQ ID NO: 2
115 <211> LENGTH: 375
116 <212> TYPE: PRT
117 <213> ORGANISM: Homo sapiens

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RAW SEQUENCE LISTING

PAPERT APPLICATION: US/09/622,439

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Input Set : A:\Y04-12-1.app

Output Set: N:\CRF3\12272000\I622439.raw

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135 <400> SEQUENCE: 2
136 Met Ala Asn Ala Ser Glu Pro Gly Gly Ser Gly Gly Gly Glu Ala Ala
137 1 5 10 15
139 Ala Leu Gly Leu Lys Leu Ala Phe Leu Ser Leu Leu Leu Cys Val Ser
140 20 25 30
142 Leu Ala Gly Asn Val Leu Phe Ala Leu Leu Ile Val Arg Glu Arg Ser
143 35 40 45
145 Leu His Arg Ala Pro Tyr Tyr Leu Leu Leu Asp Leu Cys Leu Ala Asp
146 50 55 60
148 Gly Leu Arg Ala Leu Ala Cys Leu Pro Ala Val Met Leu Ala Ala Arg
149 65 70 75 80
151 Arg Ala Ala Ala Ala Ala Gly Ala Pro Pro Gly Ala Leu Gly Cys Lys
152 85 90 95
154 Leu Leu Ala Phe Leu Ala Ala Leu Phe Cys Phe His Ala Ala Phe Leu
155 100 105 110
157 Leu Leu Gly Val Gly Val Thr Arg Tyr Leu Ala Ile Ala His His Arg
158 115 120 125
160 Phe Tyr Ala Glu Arg Leu Ala Gly Trp Pro Cys Ala Ala Met Leu Val
161 130 135 140
163 Cys Ala Ala Trp Ala Leu Ala Leu Ala Ala Phe Pro Pro Val Leu
164 145 150 155 160
166 Asp Gly Gly Gly Asp Asp Glu Asp Ala Pro Cys Ala Leu Glu Glu Arg
167 165 170 175
169 Pro Asp Gly Ala Pro Gly Ala Leu Gly Phe Leu Leu Leu Ala Val
170 180 185 190
172 Val Val Gly Ala Thr His Leu Val Tyr Leu Arg Leu Leu Phe Phe Ile
173 195 200 205
175 His Asp Arg Arg Lys Met Arg Pro Ala Arg Leu Val Pro Ala Val Ser
176 210 215 220
178 His Asp Trp Thr Phe His Gly Pro Gly Ala Thr Gly Glu Ala Ala Ala
179 225 230 235 240
181 Asn Trp Thr Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Ala Leu Val
182 245 250 255
184 Gly Ile Arg Pro Ala Gly Pro Gly Arg Gly Ala Arg Arg Leu Leu Val
185 260 265 270
187 Leu Glu Glu Phe Lys Thr Glu Lys Arg Leu Cys Lys Met Phe Tyr Ala
188 275 280 285
190 Val Thr Leu Leu Phe Leu Leu Leu Trp Gly Pro Tyr Val Val Ala Ser
191 290 295 300
193 Tyr Leu Arg Val Leu Val Arg Pro Gly Ala Val Pro Glu Ala Tyr Leu
194 305 310 315 320
196 Thr Ala Ser Val Trp Leu Thr Phe Ala Glu Ala Gly Ile Asn Pro Val
197 325 330 345
199 Val Cys Phe Leu Phe Asn Arg Glu Leu Arg Asp Cys Phe Arg Ala Glu
200 340 345 350
202 Phe Pro Cys Cys Glu Ser Pro Arg Thr Thr Glu Ala Thr His Pro Cys
203 355 360 365
205 Asp Leu Lys Gly Ile Gly Leu
206 370 375

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RAW SEQUENCE LISTING

PARENT APPLICATION: US/09/622,439

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Input Set : A:\Y04-12-1.app

Output Set: N:\CRF3\12272000\I622439.raw

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209 <210> SEQ ID NO: 3
210 <211> LENGTH: 1113
211 <212> TYPE: DNA
212 <213> ORGANISM: Homo sapiens
213 <214> FEATURE:
214 <215> NAME/KEY: CDS
215 <216> LOCATION: (1)..(1113)
216 <217> OTHER INFORMATION: SREB2
217 <218> SEQUENCE: 1
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221 Met Ala Asn Tyr Ser His Ala Ala Asp Asn Ile Leu Gln Asn Leu Ser
222 1 5 10 15
223 cct cta aca gcc ttt ctg aca ctg act tcc ttg ggt ttc ata ata gga 96
224 Pro Leu Thr Ala Phe Leu Lys Leu Thr Ser Leu Gly Phe Ile Ile Gly
225 20 25 30
226 gtc aac gtg gtg ggc aac ctc ctg atc tcc att ttg cta gta aaa gat 144
227 Val Ser Val Val Gly Asn Leu Leu Ile Ser Ile Leu Leu Val Lys Asp
228 35 40 45
229 aag acc ttg cat aca gca cct taa taa tta ctg ttg gat ctt tgc tat 192
230 Lys Thr Leu His Arg Ala Pro Tyr Tyr Phe Leu Leu Asp Leu Cys Cys
231 50 55 60
232 tca gat atc ctc aga tct aca att tgt ttc cca ttt gta ttc aac tct 240
233 Ser Asp Ile Leu Arg Ser Ala Ile Cys Phe Pro Phe Val Phe Asn Ser
234 65 70 75 80
235 gtc aca aat gac tct acc tgg act tat gga act ctg act tgc aaa gtg 288
236 Val Lys Asn Gly Ser Thr Trp Thr Tyr Gly Thr Leu Thr Cys Lys Val
237 85 90 95
238 att gcc ttt ctg ggg gtt ttg tcc tgt ttc caa act gct ttc atg ctc 336
239 Ile Ala Phe Leu Gly Val Leu Ser Cys Phe His Thr Ala Phe Met Leu
240 100 105 110
241 ttc tgc atc aat gtc acc aga taa tta gct atc gcc cat caa cgc ttc 384
242 Phe Cys Ile Ser Val Thr Arg Tyr Leu Ala Ile Ala His His Arg Phe
243 115 120 125
244 tat aca aag agg ctg acc ttt tgg acg tgt ctg gct gtg atc tgt atg 432
245 Tyr Thr Lys Arg Leu Thr Phe Trp Thr Cys Leu Ala Val Ile Cys Met
246 130 135 140
247 atg tgg act ctg tct gta gcc atg gca ttt ccc ccg gtt tta gac gtg 480
248 Val Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Leu Asp Val
249 145 150 155 160
250 ggc act taa tca ttc att agg gag gaa gal caa tgc acc ttc caa caa 528
251 Gly Thr Tyr Ser Phe Ile Arg Gln Gln Asp Gln Cys Thr Phe Gln His
252 165 170 175
253 cgc tcc ttc aag gct aat gat tcc tta gga ttt atg ctg ctt ctt gct 576
254 Arg Ser Phe Arg Ala Asn Asp Ser Leu Gly Phe Met Leu Leu Leu Ala
255 180 185 190
256 ctc atc ctc cta gcc aca cag ctt gtc taa ctc aag ctg ata ttt ttc 624
257 Leu Ile Leu Leu Ala Thr Gln Leu Val Tyr Leu Lys Leu Ile Phe Phe
258 195 200 205
259 gtc caa gat cga aga aaa atg aag cca gtc cag ttt gta gca gca gtc 672

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Input Set : A:\Y04-12-1.app

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273 Val His Asp Arg Arg Lys Met Lys Pro Val Gln Phe Val Ala Ala Val
274      210      215      220
276 aac caa aac tgg act ttt cat ggt cct gga gcc agt ggc caa gca gct 720
277 Ser Gln Asn Asp Thr Phe His Gly Pro Gly Ala Ser Gly Gln Ala Ala
278 225      230      235      240
280 gcc aat tga cta gca gga ttt gga agg ggt ccc aca cca ccc acc ttg 768
281 Ala Asn Trp Leu Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Thr Leu
282      245      250      255
284 ctg ggc atc aag caa aat gca aac acc aca ggc aqa aqa aag cta ttg 816
285 Leu Gly Ile Arg Gln Asn Ala Asn Thr Thr Gly Arg Arg Arg Leu Leu
286      260      265      270
288 gtc tta gac gaa ttc aaa atg gaa aaa aga atc aac aqa atg ttc tat 864
289 Val Leu Asp Gln Phe Lys Met Gln Lys Arg Ile Ser Arg Met Phe Tyr
290      275      280      285
292 ata atg act ttt ctg ttt cta acc ttg tgg ggc ccc tac ctg gta gcc 912
293 Ile Met Thr Phe Leu Phe Leu Thr Leu Trp Gly Pro Tyr Leu Val Ala
294      290      295      300
296 tgt tat tgg aag gtt ttt gca aag agt cct ata cta cca gga gaa ttt 960
297 Cys Tyr Trp Arg Val Phe Ala Arg Gly Pro Val Val Pro Gly Gly Phe
298 305      310      315      320
300 cta aca gct gct atc tga atg aat ttt gcc caa gca gaa atc aat cct 1008
301 Leu Thr Ala Ala Val Trp Met Ser Phe Ala Gln Ala Gly Ile Asn Pro
302      325      330      335
304 ttt gtc tgc att ttc tca aac agg gaa ctg aag cgc tgt ttc agc aca 1056
305 Phe Val Cys Ile Phe Ser Asn Arg Gln Leu Arg Arg Cys Phe Ser Thr
306      340      345      350
308 acc ctt ctt tac tgc aga aac tcc aag tta cca aag gaa cct tac tgt 1104
309 Thr Leu Leu Tyr Cys Arg Lys Ser Arg Leu Pro Arg Gln Pro Tyr Cys
310      355      360      365
312 gtt ata tga 1113
313 Val Ile
314      370
317 <210> SEQ ID NO: 4
318 <211> LENGTH: 370
319 <212> TYPE: FRT
320 <213> ORGANISM: Homo sapiens
322 <400> SEQUENCE: 4
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326 Pro Leu Thr Ala Phe Leu Lys Leu Thr Ser Leu Gly Phe Ile Ile Gly
327      20      25      30
329 Val Ser Val Val Gly Asn Leu Leu Ile Ser Ile Leu Leu Val Lys Asp
330      35      40      45
332 Lys Thr Leu His Arg Ala Pro Tyr Tyr Phe Leu Leu Asp Leu Cys Cys
333      50      55      60
335 Ser Asp Ile Leu Arg Ser Ala Ile Cys Phe Pro Phe Val Phe Asn Ser
336      65      70      75      80
338 Val Lys Asn Gly Ser Thr Trp Thr Tyr Gly Thr Leu Thr Cys Lys Val
339      85      90      95

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/622,439

DATE: 12/27/2000

TIME: 13:41:02

Input Set : A:\Y04-12-1.app

Output Set: N:\CRF3\12272000\I622439.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date